

Figure 1 (SEQ ID NO:1)

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1  ATGAAGAAAC ATCTTAAAC AGTTGCCTTG ACCCTCACTA CAGTATCGGT AGTCACCCAC
61  AATCAGGAAG TTTTTAGTTT AGTCAAAGAG CCAATTCTTA AACAACTCA AGCTTCTTCA
121 TCGATTCTTG GCGCTGACTA CGCAGAAAGT AGCGGTAAAA GCAAGTTAAA GATTAATGAA
181 ACTTCTGGCC CTGTTGATGA TACAGTCACT GACTTATTTT CGGATAAACG TACTACTCCT
241 GAAAAAATAA AAGATAATCT TGCTAAAGGT CCGAGAGAAC AAGAGTTAAA GGCAGTAACA
301 GAGAATACAG AATCAGAAAA GCAGATCACT TCTGGATCTC AACTAGAACA ATCAAAAGAG
361 TCTCTTTCTT TAAATAAAAC AGTGCCATCA ACGTCTAATT GGGAGATTGG TGATTTTATT
421 ACTAAGGGGA ATACCCTTGT TGGTCTTTCA AAATCAGGTG TTGAAAAGTT ATCTCAAAC
481 GATCATCTCG TATTGCCTAG TCAAGCAGCA GATGGAACCT AATTGATACA AGTAGCTAGT
541 TTTGCTTTTA CTCCAGATAA AAAGACGGCA ATTGCAGAAT ATACCAGTAG GGCTGGAGAA
601 AATGGGGAAA TAAGCCAAC TACCTGACGG TCTTGA AAAA ATAGAATCAG AAGCTTTTAC AGGAAATCCA
661 TTTAATTCTT ATCTACTAAA GAAGGTAACA ATCCCAACTG GTTATAACA TATTGGTCAA
721 GATGCTTTTG TGGACAATAA GAATATTGCT GAGGTTAATC TTCCTGAAAG CCTCGAGACT
781 ATTTCTGACT ATGCTTTTGC TCACCTAGCT TTGAAACAGA TCGATTTGCC AGATAATTTA
841 AAAGCGATTG GAGAATTAGC TTTTTTTGAT AATCAAATTA CAGGTAAACT TTCTTTGCCA
901 CGTCAGTTAA TGCGATTAGC AGAACGTGCT TTTAAATCAA ACCATATCAA AACAATTGAG
961 TTTAGAGGAA ATAGTCTAAA AGTGATAGGG GAAGCTAGTT TTCAAGATAA TGATCTGAGT
1021 CAACTAATGC TACCTGACGG TCTTGA AAAA ATAGAATCAG AAGCTTTTAC AGGAAATCCA
1081 GAGATGATC ACTACAATAA CCGTGTGTGT TTGTGGACAA AATCTGGAAA AAATCCTTCT
1141 GGTCTTGCTA CTGAAAATAC CTATGTTAAT CCTGATAAGT CACTATGGCA GGAAAGTCCT
1201 GAGATTGATT ATACTAAATG GTTAGAGGAA GATTTTACCT ATCAAAAAA TAGTGTTACA
1261 GGTTTTTCAA ATAAAGGCTT AAAAAAGTA AAACGTAATA AAAACTTAGA AATTCCAAAA
1321 CAGCACAATG GTGTACTAT TACTGAAATT GGTGATAATG CTTTTCGCAA TGTTGATTTT
1381 CAAAATAAAA CTTTACGTAA ATATGATTTG GAAGAAGTAA AGCTTCCCTC AACTATTCGG
1441 AAAATAGGTG CTTTGTCTTT TCAATCTAAT AACTTGAAAT CTTTGAAGC AAGTGACGAT
1501 TTAGAAGAGA TTAAAGAGGG AGCCTTTATG AATAATCGTA TTGAAACCTT GGAATTAAAA
1561 GATAAATTAG TTACTATTGG TGATGCGGCT TTCCATATTA ATCATATTTA TGCCATTGTT
1621 CTTCCAGAAAT CTGTACAAGA AATAGGGCGT TCAGCATTTT GCACAAATGG TGCAAAATAA
1681 CTTATTTTTA TGGGAAGTAA GGTAAAGACC TTAGGTGAGA TGGCATTTTT ATCAAATAGA
1741 CTTGAACATC TGGATCTTTC TGAGCAAAAA CAGTTAACAG AGATTCCTGT TCAAGCCTTT
1801 TCAGACAATG CCTTGAAAGA AGTATTATTA CCAGCATCAC TGA AACGAT TCGAGAAGAA
1861 GCCTTCAAAA AGAATCATTT AAAACAACCTG GAAGTGGCAT CTGCCTTGTC CCATATTGCT
1921 TTTAATGCTT TAGATGATAA TGATGGTGAT GAACAATTTG ATAATAAAGT GGTGTGTTAA
1981 ACGCATCATA ATTCTACGCG ACTAGCAGAT GGTGAGCATT TTATCGTTGA TCCAGATAAG
2041 TTATCTTCTA CAATAGTAGA CCTTGAAAAG ATTTTAAAC TAATCGAAGG TTTAGATTAT
2101 TCTACATTAC GTCAGACTAC TCAAACTCAG TTTAGAGACA TGACTACTGC AGGTAAAGCG
2161 TTGTTGTCAA AATCTAACCT CCGACAAGGA GAAAAACAAA AATTCCTTCA AGAAGCACAA
2221 TTTTTCCTTG GCCGCGTTGA TTTGGATAAA GCCATAGCTA AAGCTGAGAA GGCTTTAGTG
2281 ACCAAGAAGG CAACAAAGAA TGGTCAGTTG CTTGAAAGAA GTATTAACAA AGCGGTATTA
2341 GCTTATAATA ATAGCGCTAT TAAAAAGCT AATGTTAAGC GCTTGAAAAA AGAGTTAGAC
2401 TTGCTAACAG GATTAGTTGA GGGAAAAGGA CCATTAGCGC AAGCTACAAT GGTACAAGGA
2461 GTTTATTTAT TAAAGACGCC TTTGCCATTG CCAGAATATT ATATCGGATT GAACGTTTAT
2521 TTTGACAAGT CTGAAAAATT GATTTATGCA CTTGATATGA GTGATACTAT TGGCGAGGGA
2581 CAAAAAGACG CTTATGGTAA TCCTATATTA AATGTTGACG AGGATAATGA AGGTTATCAT
2641 GCCTTGGCAG TTGCCACTTT AGCTGATTAT GAGGGGCTCG ACATCAAAAC AATTTTAAAT
2701 AGTAAGCTTA GTCAATTAAC ATCTATTCTG CAGGTACCGA CTGCAGCCTA TCATAGAGCC
2761 GGTATTTTCC AAGCTATCCA AAATGCAGCG GCAGAAGCAG AGCAGTTATT GCCTAAACCA
2821 GGTACGCACT CTGAGAAGTC AAGCTCAAGT GAATCTGCTA ACTCTAAAGA TAGAGGATTG
2881 CAATCAAACC CAAAAACGAA TAGAGGACGA CACTCTGCAA TATTGCCTAG GACAGGGTCA
2941 AAAGGCAGCT TTGTCTATGG AATCTTAGGT TACACTAGCG TTGCTTTACT GTCATAATA
3001 ACTGCTATAA AAAAGAAAAA ATATTAA

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Figure 2 (SEQ ID NO:2)

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1  MKKHLKTVAL TLTTVSVVTH NQEVFSLVKE PILKQTQASS SISGADYAES SGKSKLKINE
61 TSGPVDDTVT DLFSDKRTTP EKIKNLAKG PREQELKAVT ENTESEKQIT SGSQLEQSKE
121 SLSLNKTVPS TSNWEICDFI TKGNTLVGLS KSGVEKLSQT DHLVLPSQAA DGTQLIQVAS
181 FAFTPDKKTA IAEYTSRAGE NGEISQLDVD GKEIINEGEV FNSYLLKKVT IPTGYKHIGQ
241 DAFVDNKNIA EVNLPESET ISDYAFAPLA LKQIDLPDNL KAIGELAFFD NQITGKLSLP
301 RQLMRLAERA FKSNIHKTIE FRGNSLKVIG EASFQDNDLS QLMLPDGLEK IESEFTGNP
361 GDDHYNNRVV LWTKSGKNPS GLATENTYVN PDKSLWQESP EIDYTKWLEE DFTYQKNSVT
421 GFSNKGLOKV KRKNLEIPK QHNGVTITEI GDNAFRNVDF QNKTLRKYDL EEVKLPSTIR
481 KIGAFQSN NLKSFEASDD LEEIKGAFM NNRIETLELK DKLVTIGDAA FHINHIYAIV
541 LPESVQEIGR SAFRQNGANN LIFMGSKVKT LGEMAFLSNR LEHLDLSEQK QLTEIPVQAF
601 SDNALKEVLL PASLKTIREE AFKKNHLKQL EVASALSHIA FNALDDNDGD EQFDNKVVVK
661 THHNSYALAD GEHFIVDPDK LSSTIVDLEK ILKLIEGLDY STLRTTQTQ FRDMTTAGKA
721 LLSKSNLRQG EKQKFLQEAQ FFLGRVDLDK AIAKAEKALV TKKATKNGQL LERSINKAVL
781 AYNNSAIKKA NVKRLEKELD LLTGLVEGKG PLAQATMVQG VYLLKTPLPL PEYYIGLNVY
841 FDKSGKLIYA LDMSDTIGEG QKDAYGNPIL NVDEDNEGYH ALAVATLADY EGLDIKTILN
901 SKLSQLTSIR QVPTAAYHRA GIFQAIQNAA AEAEQLLPKP GTHSEKSSSS ESANSKDRGL
961 QSNPKTNRGR HSAILPRTGS KGSFVYGILG YTSVALLSLI TAIKKKKY*
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Figure 3

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned.. Alignment Score = 118839  
Gaps Inserted = 0 Conserved Identities = 936

Pairwise Alignment Mode: Fast

Pairwise Alignment Parameters:

ktup = 1 Gap Penalty = 3 Top Diagonals = 5 Window Size = 5

Multiple Alignment Parameters:

Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1

Delay Divergent = 40% Gap Distance = 8

Similarity Matrix: blosum

Processing time: 12.9 seconds

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Spy74_M3      1                      DYAES      5
Spy70_M5      1                      LVKEPILKQTQASSSISGADYAES 24
Spy69_M6      1                      KQTQASSSISGADYAES 17
Spy68_M2      1                      LVKEPILKQTQASSSISGADYAES 24
Spy60_M1      1                      LVKEPILKQTQASSSISGADYAES 24
12357_M18     1                      VKEPILKQTQASSSISGADYAES 23
700294_M1     1 MKKHILKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES 50
                                     *****

Spy74_M3      6 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 55
Spy70_M5      25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
Spy69_M6      18 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 67
Spy68_M2      25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
Spy60_M1      25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
12357_M18     24 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 73
700294_M1     51 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 100
      *****

Spy74_M3      56 ENTESEKQITSGSQLEQSKESLSLNKRVFPSTSNWEICDFITKGNLVLGSL 105
Spy70_M5      75 ENTESEKQINSGSQLEQSKESLSLNKRVFPSTSNWEICDFITKGNLVLGSL 124
Spy69_M6      68 ENTESEKQINSGSQLEQSKESLSLNKRVFPSTSNWEICDFITKGNLVLGSL 117
Spy68_M2      75 ENTESEKQITSGSQLEQSKESLSLNKIVPSTSNWEICDFITKGNLVLGSL 124
Spy60_M1      75 ENTESEKQITSGSQLEQSKESLSLNKIVPSTSNWEICDFITKGNLVLGSL 124
12357_M18     74 ENTESEKQINSGSQLEQSKESLSLNKRVFPSTSNWEICDFITKGNLVLGSL 123
700294_M1     101 ENTESEKQITSGSQLEQSKESLSLNKIVPSTSNWEICDFITKGNLVLGSL 150
      *****

Spy74_M3      106 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 155
Spy70_M5      125 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
Spy69_M6      118 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 167
Spy68_M2      125 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
Spy60_M1      125 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
12357_M18     124 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 173
700294_M1     151 KSGVEKLSQTDHLVLPSSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 200
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Spy74_M3	156	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	205
Spy70_M5	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy69_M6	168	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	217
Spy68_M2	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy60_M1	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
12357_M18	174	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	223
700294_M1	201	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	250

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Spy74_M3	206	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	255
Spy70_M5	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy69_M6	218	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	267
Spy68_M2	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy60_M1	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
12357_M18	224	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	273
700294_M1	251	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	300

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Spy74_M3	256	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	305
Spy70_M5	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy69_M6	268	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	317
Spy68_M2	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy60_M1	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
12357_M18	274	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	323
700294_M1	301	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	350

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Spy74_M3	306	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	355
Spy70_M5	325	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy69_M6	318	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	367
Spy68_M2	325	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy60_M1	325	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
12357_M18	324	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	373
700294_M1	351	IESEAFTEGPNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	400

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Spy74_M3	356	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	405
Spy70_M5	375	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	424
Spy69_M6	368	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	417
Spy68_M2	375	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	424
Spy60_M1	375	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	424
12357_M18	374	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	423
700294_M1	401	EIDYTKWLEEDFTYQKNSVTGFSKGLQKVKNKNLEIPKQHNGVTITEI	450

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Spy74_M3	406	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	455
Spy70_M5	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy69_M6	418	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	467
Spy68_M2	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
Spy60_M1	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	474
12357_M18	424	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	473
700294_M1	451	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNNLKSFEASDD	500

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Spy74_M3	456	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	505
Spy70_M5	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	524
Spy69_M6	468	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	517
Spy68_M2	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	524
Spy60_M1	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	524
12357_M18	474	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	523
700294_M1	501	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIIYAIVLPESVQEIQR	550

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Spy74_M3	506	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	555
Spy70_M5	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy69_M6	518	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	567
Spy68_M2	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy60_M1	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
12357_M18	524	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	573
700294_M1	551	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	600

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Spy74_M3	556	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	605
Spy70_M5	575	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	624
Spy69_M6	568	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	617
Spy68_M2	575	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	624
Spy60_M1	575	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	624
12357_M18	574	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	623
700294_M1	601	SDNALKEVLLPASLKTIREEFKKNHLKQLEVASALSHTAFNALDDNDGD	650

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Spy74_M3	606	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	655
Spy70_M5	625	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
Spy69_M6	618	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	667
Spy68_M2	625	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
Spy60_M1	625	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
12357_M18	624	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	673
700294_M1	651	EQFDNKVVVKTHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	700

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Spy74_M3	656	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	705
Spy70_M5	675	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	724
Spy69_M6	668	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	717
Spy68_M2	675	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	724
Spy60_M1	675	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	724
12357_M18	674	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	723
700294_M1	701	STLRQTTQTQFRDMTTAGKALLSKSLRQGEKQKFLQEAQFFLGRVDLDK	750

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Spy74_M3	706	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	755
Spy70_M5	725	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy69_M6	718	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	767
Spy68_M2	725	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy60_M1	725	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
12357_M18	724	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	773
700294_M1	751	AIKAKEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	800

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